STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 10 820,067
Source: TEWO
Date Processed by STIC: 1-31-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450. Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street.
   Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/820,067

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .); this will
                          prevent "wrapping."

2____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers:
      Numbering   use space characters, instead.

4____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                           ensure your subsequent submission is saved in ASCII text.

5____ Variable Length   Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                           each n or Xaa can only represent a single residue. Please present the maximum number of each
                           residue having variable length and indicate in the <220>-<223> section that some may be missing

6____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                           previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                           the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                           Artificial or Unknown sequences.

7____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
                           (i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
                           (ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
                           This sequence is intentionally skipped

                           Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8   Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
      (NEW RULES)   <210> sequence id number
                           <400> sequence id number
                           000

9   Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.821 of Sequence Rules, use of <220> <221> is MANDATORY if n's or Xaa's are present
                           In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10.____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or
        Response   scientific name (Genus/species) <220> <221> section is required when <213> response is Unknown or
                           is Artificial Sequence

11.____ Use of <220>   Sequence(s) ____ missing the <220> section and associated numeric identifiers and responses
                           Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                           "Unknown." Please explain source of genetic material in <220> to <223> section.
                           (See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                           listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can only represent a single nucleotide: "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067 TIME: 11:27:02

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

```
 4 <110> APPLICANT: Fletchner, J.
 5         Prince-Cohane, K.
 6         Mehta, S.
 7         Slusarewicz, P.
 8         Andjelic, S.
 9         Barber, B.
11 <120> TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
12         VACCINES AND IMMUNOTHERAPIES
15 <130> FILE REFERENCE: 8449-406-999
17 <140> CURRENT APPLICATION NUMBER: 10/820,067
18 <141> CURRENT FILING DATE: 2004-04-08
20 <150> PRIOR APPLICATION NUMBER: 60/462,469
21 <151> PRIOR FILING DATE: 2003-04-11
23 <150> PRIOR APPLICATION NUMBER: 60/463,746
24 <151> PRIOR FILING DATE: 2003-04-18
26 <150> PRIOR APPLICATION NUMBER: 60/503,417
27 <151> PRIOR FILING DATE: 2003-09-16
29 <160> NUMBER OF SEQ ID NOS: 926
31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 4
35 <212> TYPE: PRT
36 <213> ORGANISM: Malaria
38 <400> SEQUENCE: 1
39 Asn Ala Asn Pro
40  1
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 9
45 <212> TYPE: PRT
46 <213> ORGANISM: Unknown
48 <220> FEATURE:
49 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 51 <221> NAME/KEY: VARIANT
52 <222> LOCATION: 2
53 <223> OTHER INFORMATION: Xaa = Leu or Met
W--> 55 <221> VARIANT
56 <222> LOCATION: 6
57 <223> OTHER INFORMATION: Xaa = Val or Ile or Leu or Thr
W--> 59 <221> VARIANT
60 <222> LOCATION: 9
61 <223> OTHER INFORMATION: Xaa = Val or Leu
W--> 63 <221> VARIANT
64 <222> LOCATION: 1,3 , 4, 5, 7, 8
```

(ps.6)

Does Not Comply
Corrected Diskette Needed
(ps. 2,3)

RAW SEQUENCE LISTING   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067   TIME: 11:27:02

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
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```
      65 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 67 <400> 2
W--> 68 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      69 1               5
      72 <210> SEQ ID NO: 3
      73 <211> LENGTH: 9
      74 <212> TYPE: PRT
      75 <213> ORGANISM: Unknown
      77 <220> FEATURE:
      78 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 80 <221> NAME/KEY: VARIANT
      81 <222> LOCATION: 2
      82 <223> OTHER INFORMATION: Xaa = Leu or Met
W--> 84 <221> VARIANT
      85 <222> LOCATION: 1, 3, 4, 5, 6, 7, 8
      86 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 88 <400> 3
W--> 89 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
      90 1               5
      93 <210> SEQ ID NO: 4
      94 <211> LENGTH: 8
      95 <212> TYPE: PRT
      96 <213> ORGANISM: Unknown
      98 <220> FEATURE:
      99 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 101 <221> NAME/KEY: VARIANT
     102 <222> LOCATION: 2
     103 <223> OTHER INFORMATION: Xaa = Val or Gln
W--> 105 <221> VARIANT
     106 <222> LOCATION: 1, 3, 4, 5, 6, 7, 8
     107 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 109 <400> 4
W--> 110 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
     111 1               5
     114 <210> SEQ ID NO: 5
     115 <211> LENGTH: 5
     116 <212> TYPE: PRT
     117 <213> ORGANISM: Unknown
     119 <220> FEATURE:
     120 <223> OTHER INFORMATION: HLA-DR peptide binding motif
     122 <400> SEQUENCE: 5
     123 Gln Lys Arg Ala Ala
     124 1               5
     127 <210> SEQ ID NO: 6
     128 <211> LENGTH: 5
     129 <212> TYPE: PRT
     130 <213> ORGANISM: Unknown
     132 <220> FEATURE:
     133 <223> OTHER INFORMATION: HLA-DR peptide binding motif
```

(handwritten annotation): 8 - Leu is at this location.

```
135 <400> SEQUENCE: 6
136 Arg Arg Arg Ala Ala
137  1               5
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 7
142 <212> TYPE: PRT
143 <213> ORGANISM: Unknown
145 <220> FEATURE:
146 <223> OTHER INFORMATION: motif in heptamiric region recognized by heat
147       shock protein
W--> 149 <221> NAME/KEY: VARIANT
150 <222> LOCATION: 2
151 <223> OTHER INFORMATION: Xaa = Trp or any amino acid
W--> 153 <221> VARIANT
154 <222> LOCATION: 1, 3, 5, 7
155 <223> OTHER INFORMATION: Xaa = hydrophobic amino acid residues
W--> 157 <221> VARIANT
158 <222> LOCATION: 4, 6
159 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 161 <400> 7
W--> 162 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
163  1               5
166 <210> SEQ ID NO: 8
167 <211> LENGTH: 7
168 <212> TYPE: PRT
169 <213> ORGANISM: Unknown
171 <220> FEATURE:
172 <223> OTHER INFORMATION: motif in heptamiric region recognized by heat
173       shock protein
W--> 175 <221> NAME/KEY: VARIANT
176 <222> LOCATION: 2
177 <223> OTHER INFORMATION: Xaa = Trp or any amino acid
W--> 179 <221> VARIANT
180 <222> LOCATION: 1, 3, 5, 7,
181 <223> OTHER INFORMATION: Xaa = hydrophobic amino acid residue, particularly
182       tryptophan, leucine or phenylalanine
W--> 184 <221> VARIANT
185 <222> LOCATION: 4, 6
186 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 188 <400> 8
W--> 189 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
190  1               5
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 4
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <221> NAME/KEY: VARIANT
200 <222> LOCATION: 1
```

See item # 11 on error summary sheet

pls explain source of genetic material.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
201 <223> OTHER INFORMATION: Xaa = Ala/Ser/Val/Lys/Glu/Gly/Leu
203 <220> FEATURE:
204 <223> OTHER INFORMATION: In the order of preference, with Ala the most preferred
206 <220> FEATURE:
207 <221> NAME/KEY: VARIANT
208 <222> LOCATION: 2
209 <223> OTHER INFORMATION: Xaa = Lys/Val/Glu
211 <220> FEATURE:
212 <223> OTHER INFORMATION: In the order of preference, with Lys the most preferred
214 <220> FEATURE:
215 <221> NAME/KEY: VARIANT
216 <222> LOCATION: 3
217 <223> OTHER INFORMATION: Xaa = Val/Ser/Phe/Thr/Lys/Ala/Glu
219 <220> FEATURE:
220 <223> OTHER INFORMATION: In the order of preference, with Val the most preferred
222 <400> SEQUENCE: 9
223 Xaa Xaa Xaa Leu
224  1
227 <210> SEQ ID NO: 10
228 <211> LENGTH: 10
229 <212> TYPE: PRT
230 <213> ORGANISM: Adeno Virus
232 <400> SEQUENCE: 10
233 Ser Gly Pro Ser Asn Thr Pro Pro Glu Ile
234  1             5                   10
237 <210> SEQ ID NO: 11
238 <211> LENGTH: 11
239 <212> TYPE: PRT
240 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
242 <400> SEQUENCE: 11
243 Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu
244  1             5                   10
247 <210> SEQ ID NO: 12
248 <211> LENGTH: 10
249 <212> TYPE: PRT
250 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
252 <400> SEQUENCE: 12
253 Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly
254  1             5                   10
257 <210> SEQ ID NO: 13
258 <211> LENGTH: 9
259 <212> TYPE: PRT
260 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
262 <400> SEQUENCE: 13
263 Arg Pro Gln Ala Ser Gly Val Tyr Met
264  1             5
267 <210> SEQ ID NO: 14
268 <211> LENGTH: 9
269 <212> TYPE: PRT
```

W--> (marking at line 223)

```
270 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
272 <400> SEQUENCE: 14
273 Phe Gln Pro Gln Asn Gly Gln Phe Ile
274 1               5
277 <210> SEQ ID NO: 15
278 <211> LENGTH: 9
279 <212> TYPE: PRT
280 <213> ORGANISM: Influenza Virus
282 <400> SEQUENCE: 15
283 Ile Glu Gly Gly Trp Thr Gly Met Ile
284 1               5
287 <210> SEQ ID NO: 16
288 <211> LENGTH: 10
289 <212> TYPE: PRT
290 <213> ORGANISM: Influenza Virus
292 <400> SEQUENCE: 16
293 Thr Tyr Val Ser Val Ser Thr Ser Thr Leu
294 1               5                10
297 <210> SEQ ID NO: 17
298 <211> LENGTH: 8
299 <212> TYPE: PRT
300 <213> ORGANISM: Influenza Virus
302 <400> SEQUENCE: 17
303 Phe Glu Ala Asn Gly Asn Leu Ile
304 1               5
307 <210> SEQ ID NO: 18
308 <211> LENGTH: 9
309 <212> TYPE: PRT
310 <213> ORGANISM: Influenza Virus
312 <400> SEQUENCE: 18
313 Ile Tyr Ser Thr Val Ala Ser Ser Leu
314 1               5
317 <210> SEQ ID NO: 19
318 <211> LENGTH: 9
319 <212> TYPE: PRT
320 <213> ORGANISM: Influenza Virus
322 <400> SEQUENCE: 19
323 Thr Tyr Gln Arg Thr Arg Ala Leu Val
324 1               5
327 <210> SEQ ID NO: 20
328 <211> LENGTH: 9
329 <212> TYPE: PRT
330 <213> ORGANISM: Influenza Virus
332 <400> SEQUENCE: 20
333 Cys Thr Glu Leu Lys Leu Ser Asp Tyr
334 1               5
337 <210> SEQ ID NO: 21
338 <211> LENGTH: 8
339 <212> TYPE: PRT
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067   TIME: 11:27:03

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,3,4,5,6,7,8,9
Seq#:3; Xaa Pos. 1,2,3,4,5,6,7,8
Seq#:4; Xaa Pos. 1,2,3,4,5,6,7
Seq#:7; Xaa Pos. 1,2,3,4,5,6,7
Seq#:8; Xaa Pos. 1,2,3,4,5,6,7
Seq#:9; Xaa Pos. 1,2,3
Seq#:401; Xaa Pos. 7
Seq#:402; Xaa Pos. 3
Seq#:407; Xaa Pos. 2,6
Seq#:454; Xaa Pos. 5
Seq#:564; Xaa Pos. 7
Seq#:565; Xaa Pos. 3
Seq#:570; Xaa Pos. 2,6
Seq#:617; Xaa Pos. 5
Seq#:805; Xaa Pos. 7
Seq#:806; Xaa Pos. 3
Seq#:811; Xaa Pos. 2,6
Seq#:858; Xaa Pos. 5

VERIFICATION SUMMARY   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067   TIME: 11:27:03

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

```
L:51  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:55  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:59  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:63  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:67  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:68  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:80  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:84  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:88  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:89  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:101 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:105 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:149 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:161 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:179 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:501 M:283 W: Missing Blank Line separator, <400> field identifier
L:4951 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4955 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:401
L:4956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:401 after pos.:0
L:4968 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4972 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:402
L:4973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:402 after pos.:0
L:5037 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:407
L:5042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:407 after pos.:0
L:5652 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5656 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:454
L:5657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:454 after pos.:0
L:7086 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7090 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:564
L:7091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:564 after pos.:0
L:7103 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:565
L:7108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:565 after pos.:0
L:7172 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:570
L:7177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:570 after pos.:0
L:7787 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
```

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```
L:7791 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:617
L:7792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:617 after pos.:0
L:10404 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10408 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:805
L:10409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:805 after pos.:0
L:10422 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10426 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:806
L:10427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:806 after pos.:0
L:10496 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10500 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:811
L:10501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:811 after pos.:0
L:11158 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:11162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:858
L:11163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:858 after pos.:0
```